

FIG. 1A

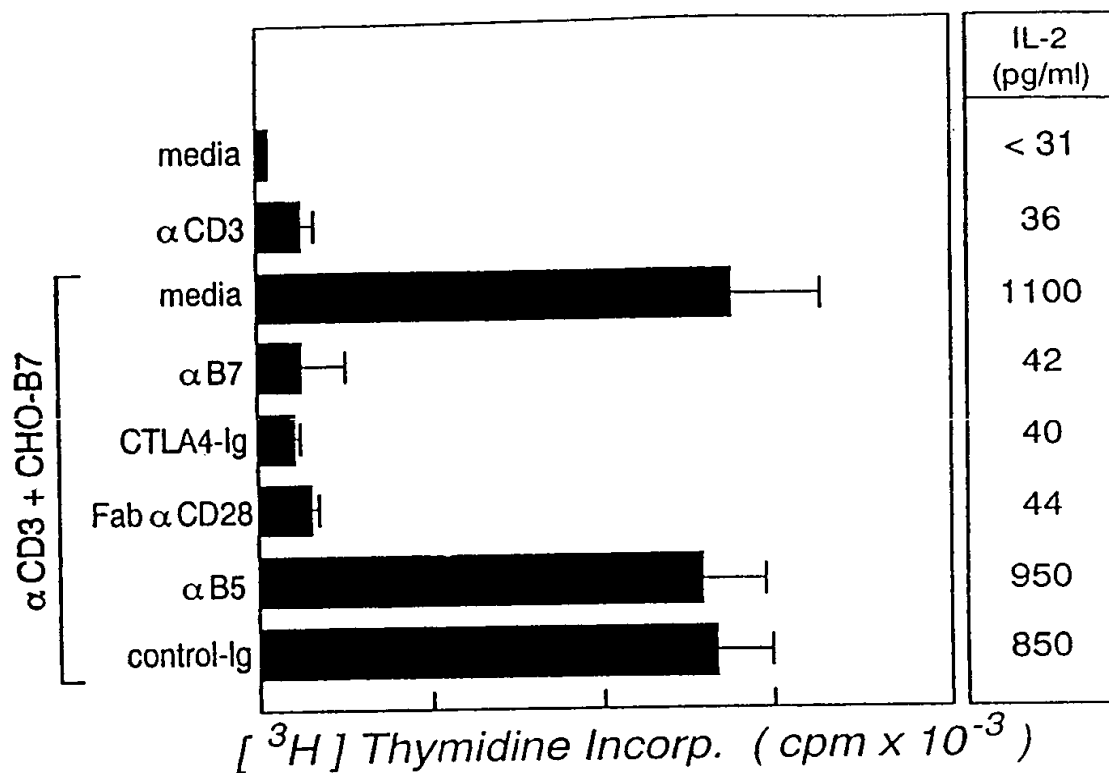


FIG. 1B

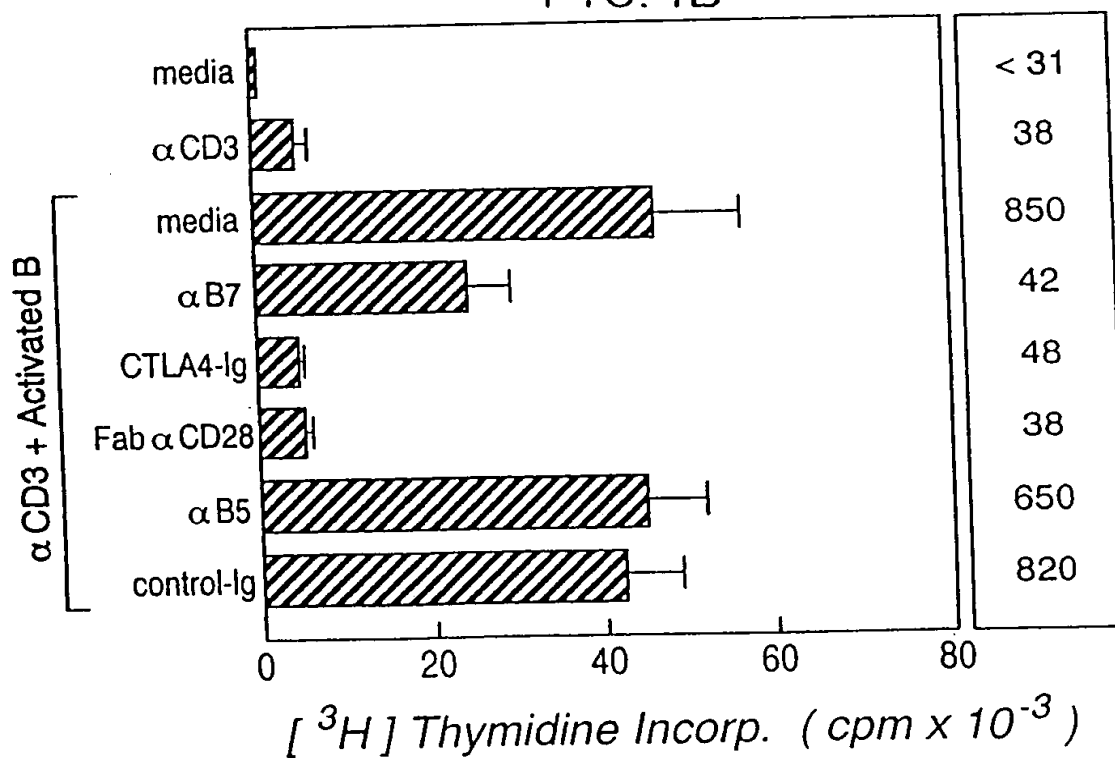


FIG. 2C

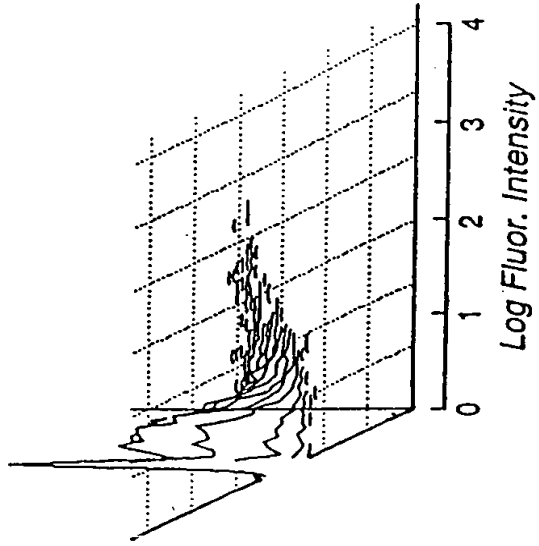


FIG. 2B

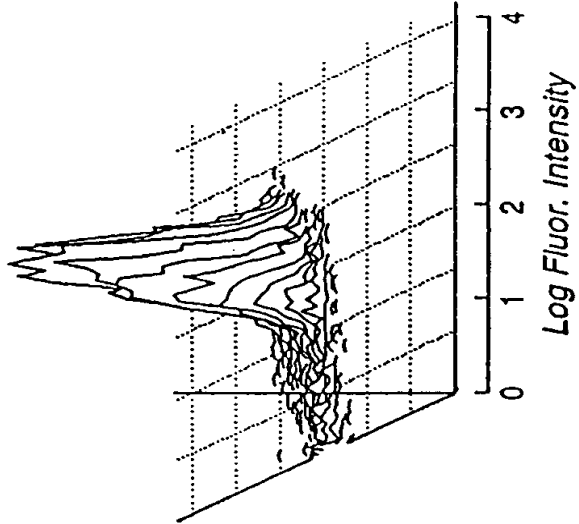


FIG. 2A

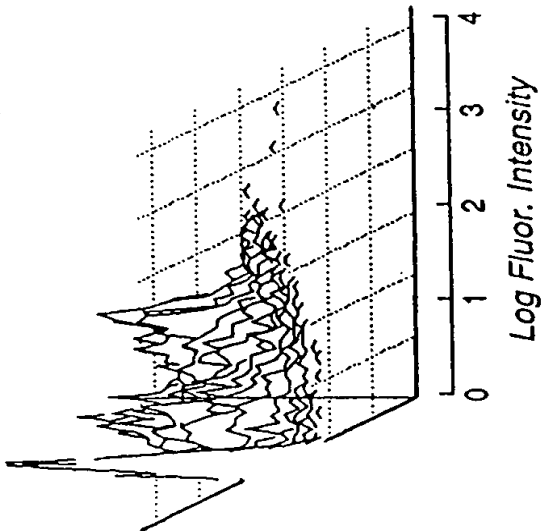


FIG. 3A

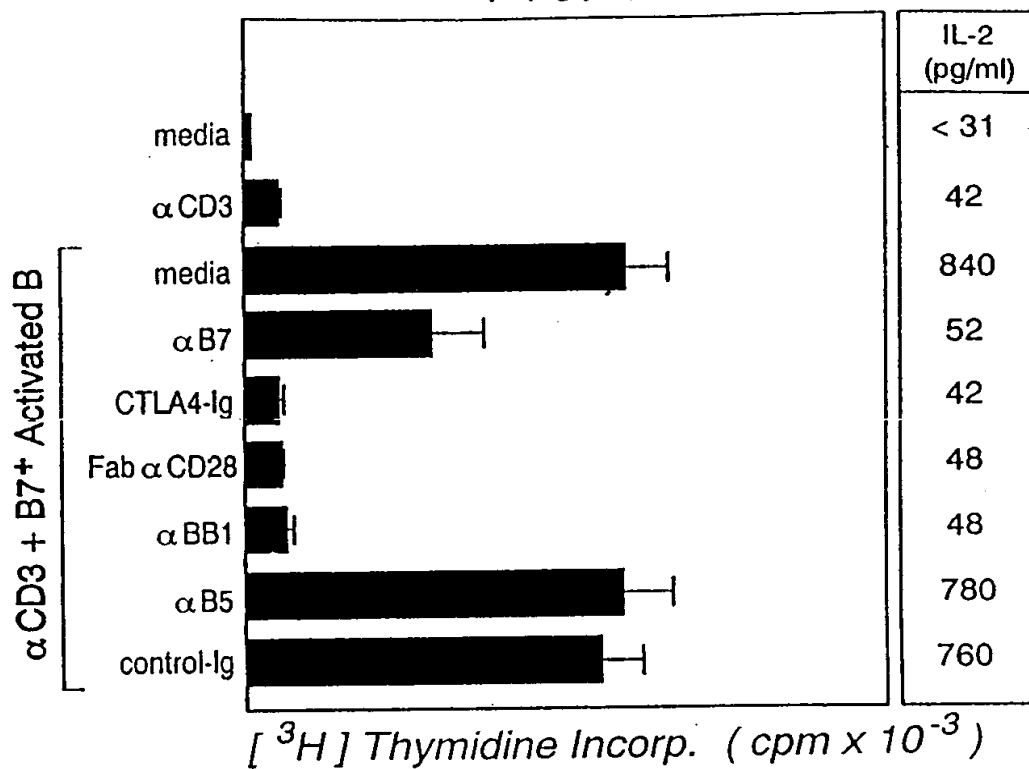
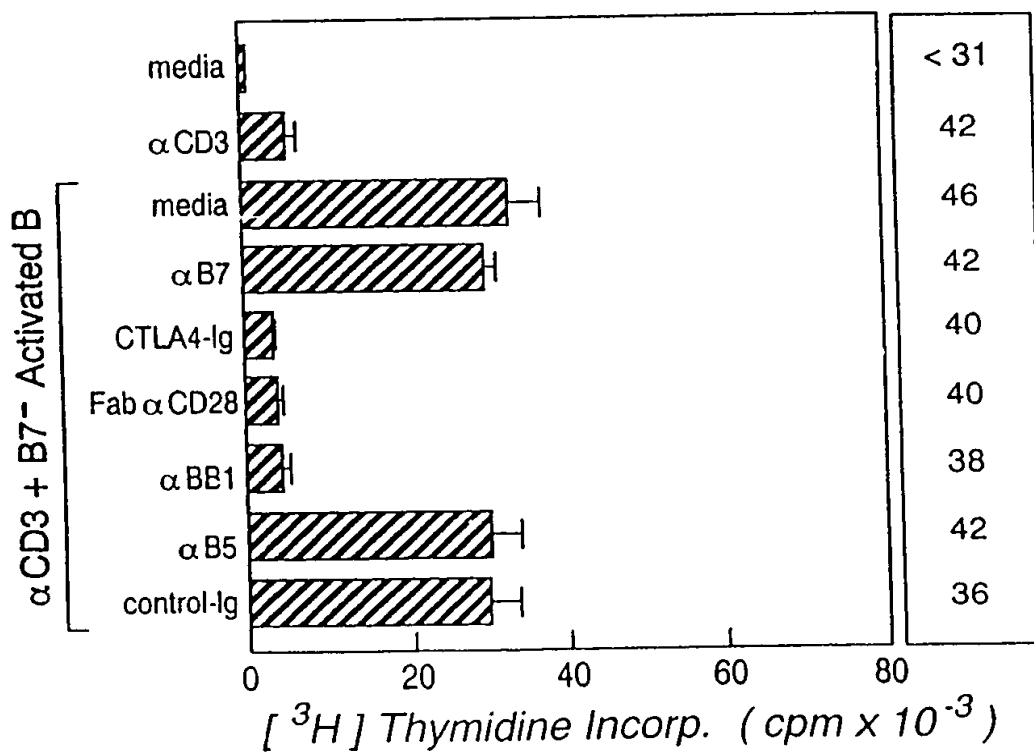


FIG. 3B



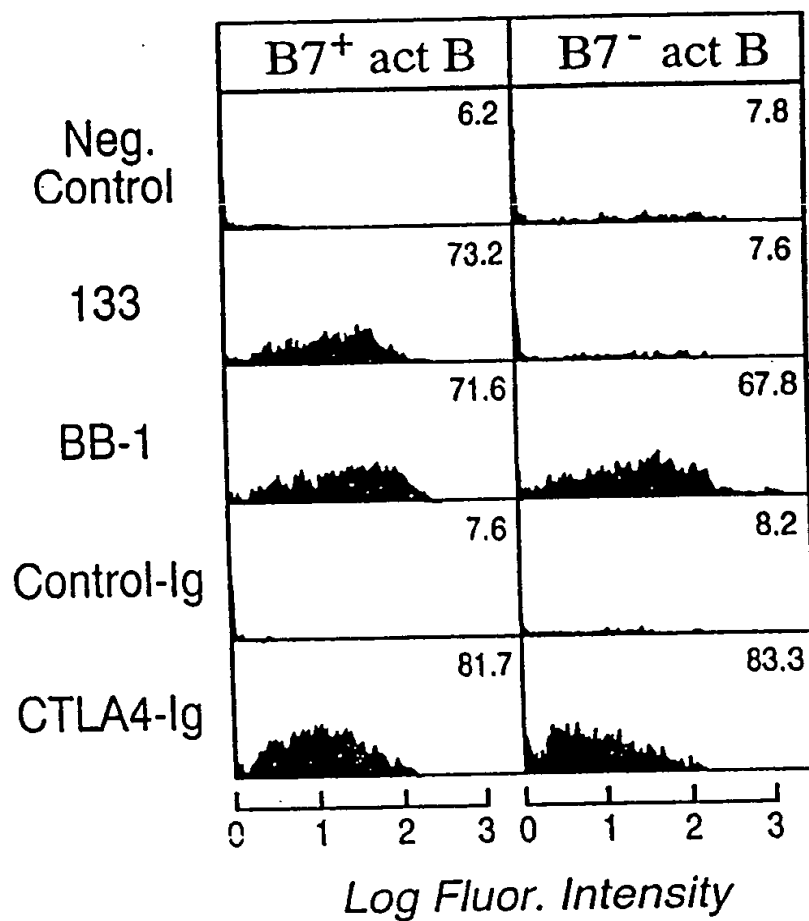
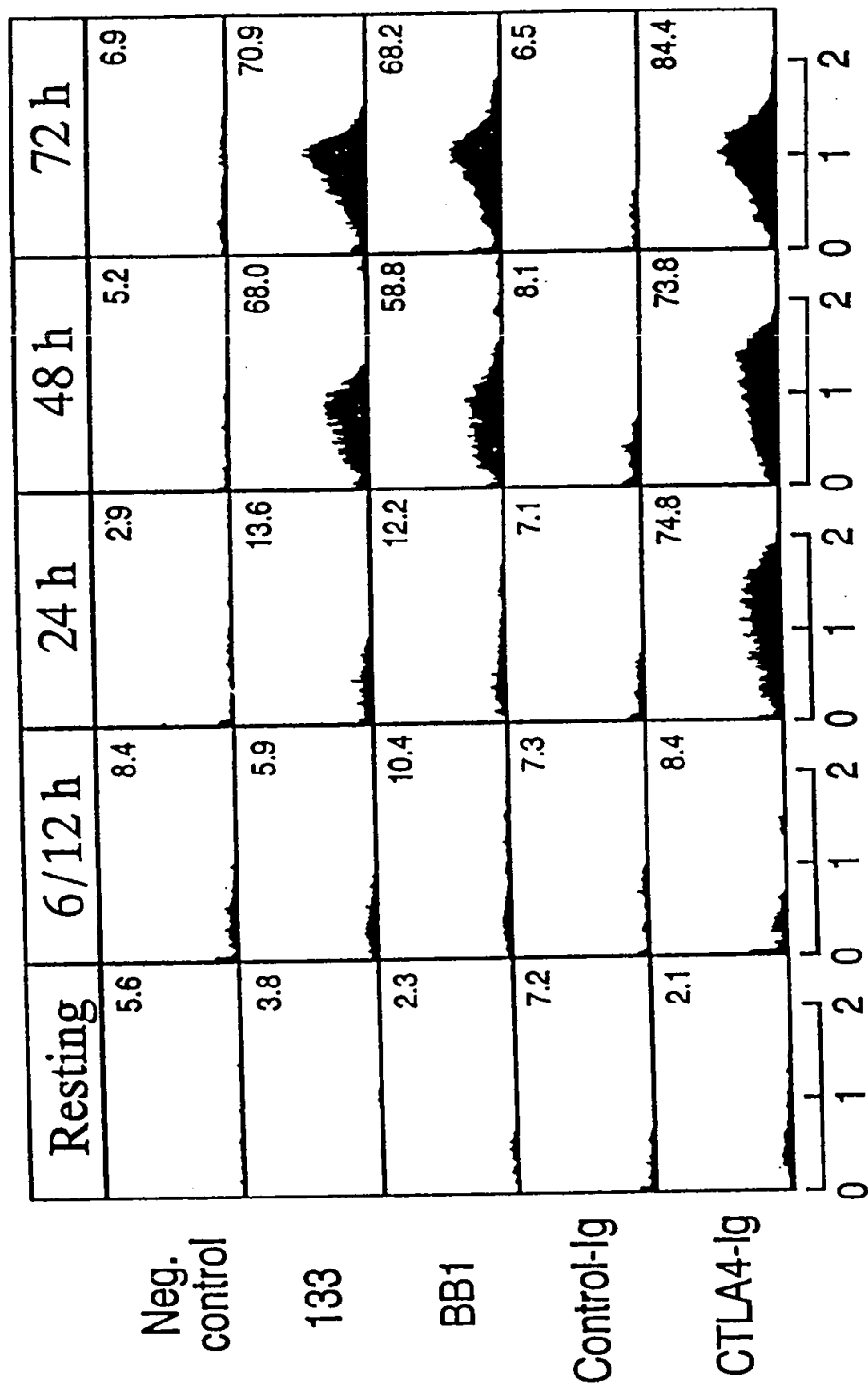


FIG. 4

# B Cells Activated by sIg Crosslinking

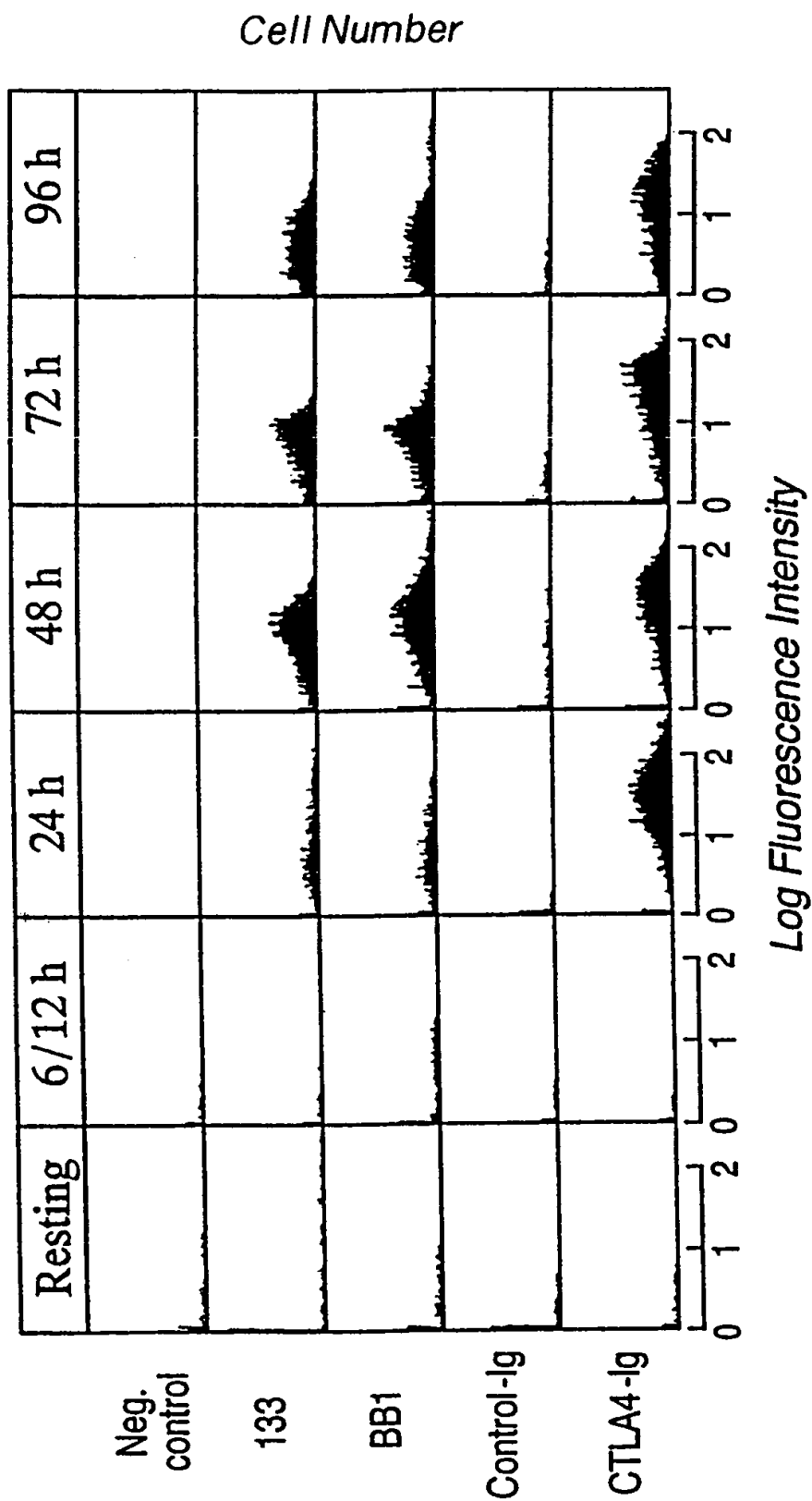


*Log Fluorescence Intensity*

FIG. 5

E/G. 6

## B Cells Activated by Class II Crosslinking



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FIG. 7A

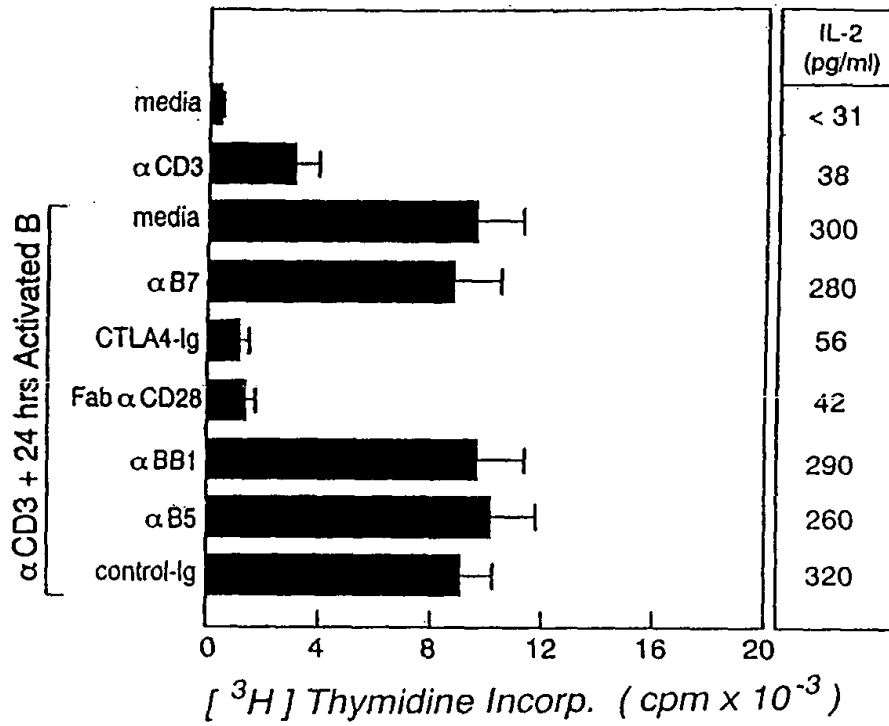


FIG. 7B

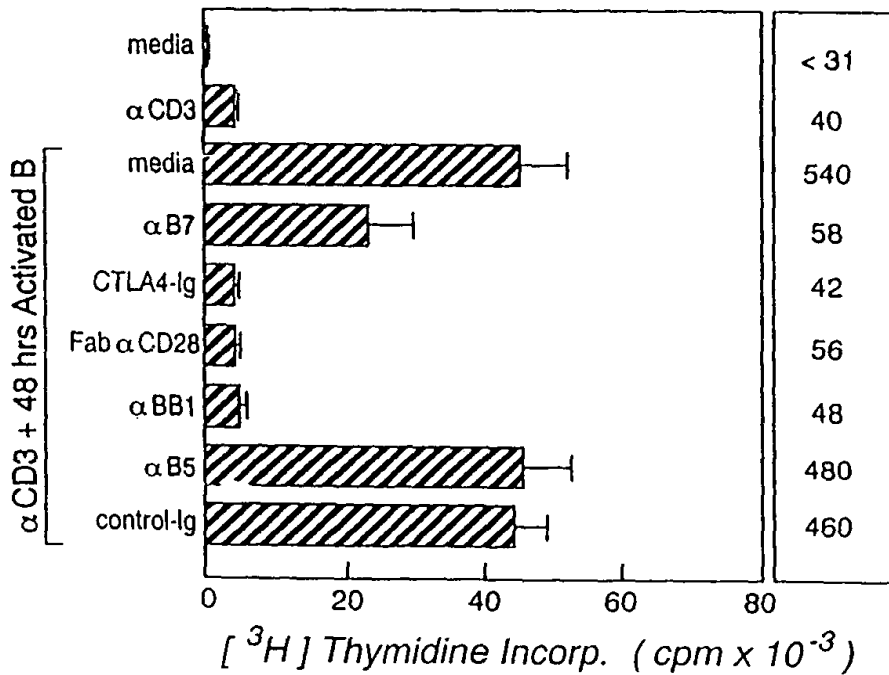




FIG. 8A

1	CACAGGGTGAAAGCTTTTGGCTTCTCTGCTGCTGTAAACAGGGACTAGCACACAGACACACACGGATGAGTGGGGTC	70
71	ATTTCCAGATATTAGGTCACAGCAGAGCAGCCAAAATGGATCCCCAGTGCACACTATGGGACTGAGTAACA	140
141	TTCTCTTTGTGATGGCCCTTCCTGCTCTCTGGTGTCTCTCTGAAAGATTCAAGCTTATTTCAATGAGAC	210
12	I L F V M A F L L S G A A P L K I Q A Y F N E T	35
	#	
211	TGCAGACCTGCCATGCCAAATTTGCAAACTCTCAAAACCAAGCCCTGAGTGAGCTAGTAGTATTTTGGCAG	280
36	A D L P C Q F A N S Q N Q S L S E L V V F W Q	58
	*	
281	GACCAGGAAAACTTGGTTCTGAATGAGGTATACTTAGGCCAAAGAGAAAATTTCACAGTGTTCATTCCCAAGT	350
59	D Q E N L V L N E V Y L G K E K F D S V H S K	81
351	ATATGGGGCCGCACAAGTTTGTATTCGGACAGTTGGACCCCTGAGACTTCACAATCTTCAGATCAAGGACAA	420
82	Y M G R T S F D S D S W T L R L H N L Q I K D K	105

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FIG. 8B

421 GGGCTTGATCAATGTATCATCCATCACAAGAGCCACAGGAATGATTCGCATCCACAGATGAATTCT 490  
106 G L Y Q C I I H H K K P T G M I R I H Q M N S 128  
491 GAACTGTCAGTGCCTAAGTTCAGTCAACCTGAAATAGTACCAATTTCTAATATAACAGAAAATGTGT 560  
129 E L S V L A N F S Q P E I V P I S N I T E N V 151  
561 ACATAAATTGACCTGCTCATCTATACACGGTTACCCAGAACCTAAGAAGATGAGTGTTTGTCTAAGAAC 630  
152 Y I N L T C S S I H G Y P E P K K M S V L L R T 175  
631 CAAGAATTCAACTATCGAGTATGATGGTATTATGCAGAAATCTCAAGATAATGTCACAGAACTGTACGAC 700  
176 K N S T I E Y D G I M Q K S Q D N V T E L Y D 198  
701 GTTCCATCAGCTTGCTGTTTCATTCCTGATGTTACGAGCAATATGACCATCTTCTGTATTCTGGAAA 770  
199 V S I S L S V S F P D V T S N M T I F C I L E 221  
771 CTGACAAGACGGGCTTTTATCTTTCACCTTCTCTATAGAGCTTGAGGACCCCTCAGCCCTCCCCAGACCA 840  
222 T D K T R L L S S P F S I E L E D P Q P P D H 245



# FIG. 8C

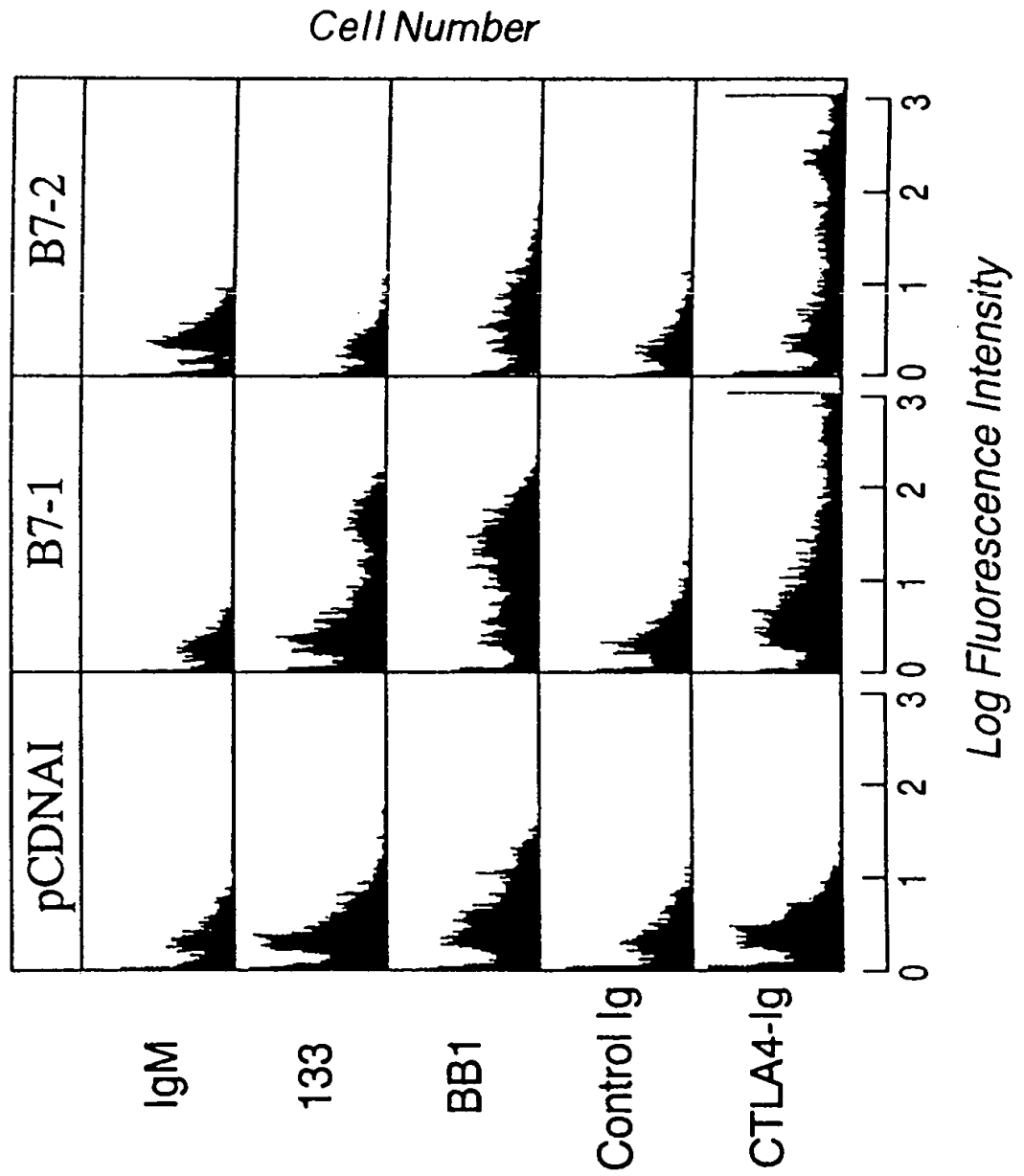
841 CATTCCTTGGATTACAGCTGTACTTCCAAACAGTATTATATGTGTGATGGTTTCTGTCTAAATCTATGG 910  
246 I P W I T A V L P T V I I C V M V F C L I L W 268

911 AA.TGGAAGAAGAAGCGCCCTCGCAACTCTTATAAATGTGGAACCAACACAATGGAGAGGGAAGAGA 980  
269 K W K K K R P R N S Y K C G T N T M E R E E 291

981 GTGAACAGACCAAGAAAAAATCCATATACCTGAAAGATCTGATGAAGCCAGCGTGTTTTAA 1050  
292 S E Q T K K R E K I H I P E R S D E A Q R V F K 315

1051 AAGTTCGAAGACATCTTCATGCGACAAAAGTGATACATGTTTAAATTAAGAGTAAGCCAAAAAAA 1120  
316 S S K T S S C D K S D T C F \* 329

FIG. 9



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FIG. 10A

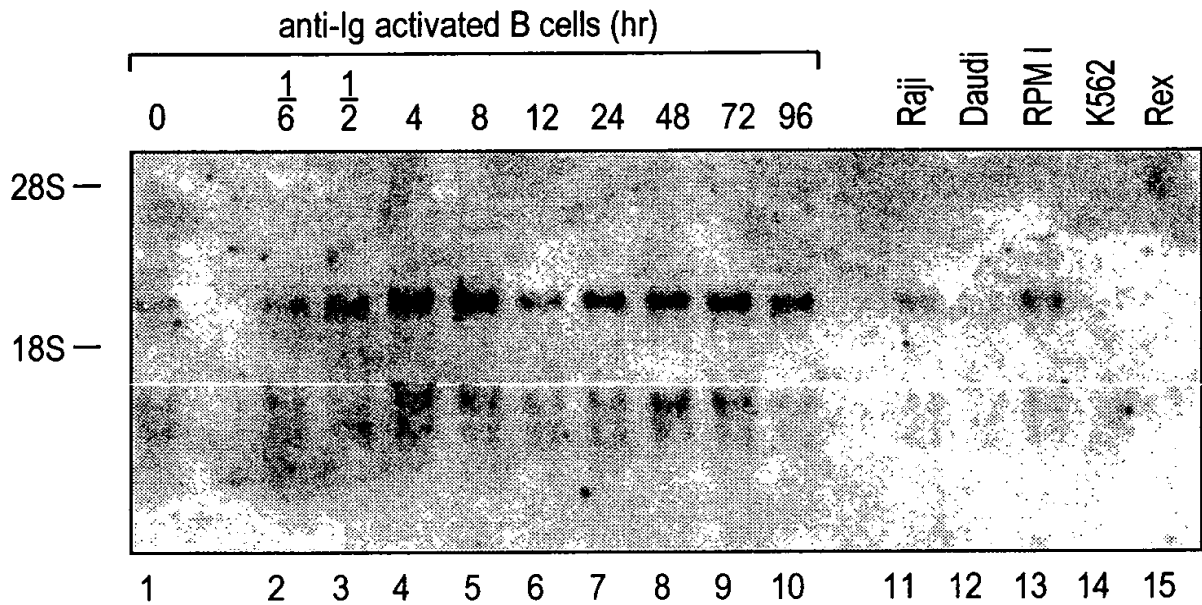
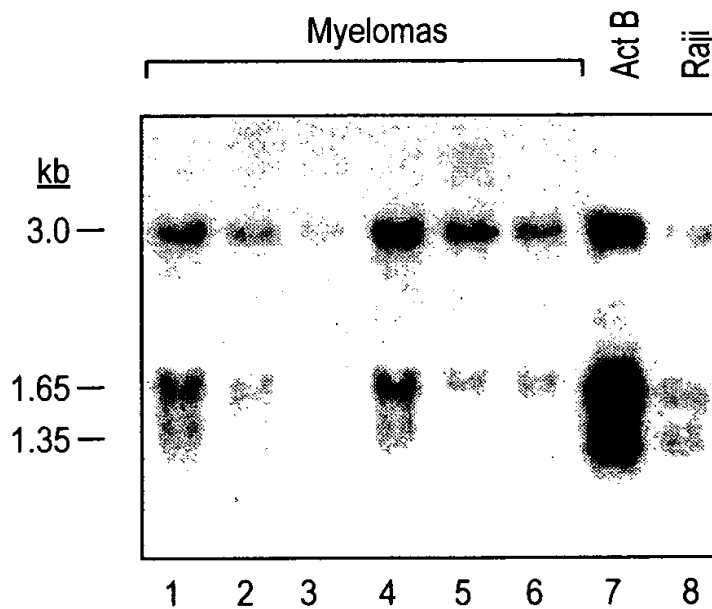


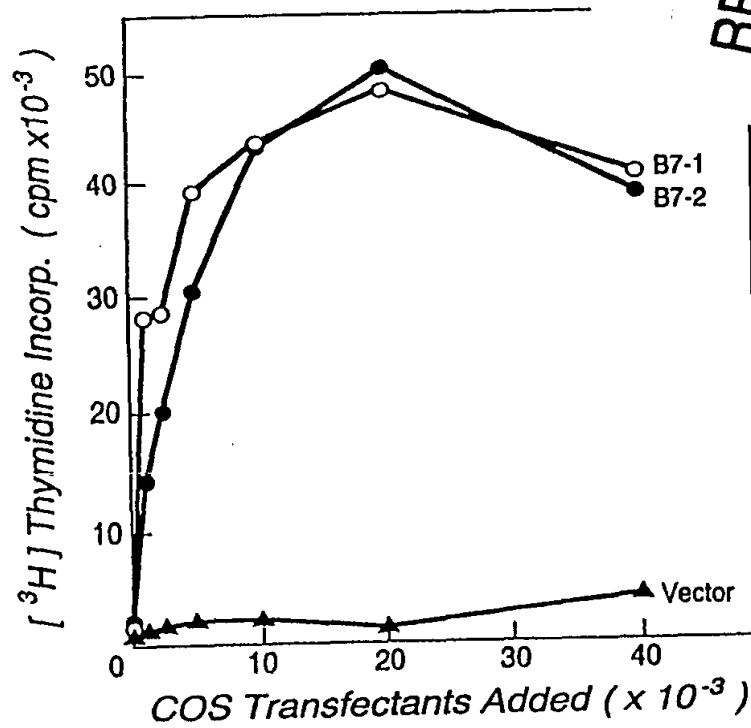
FIG. 10B





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FIG. 11A

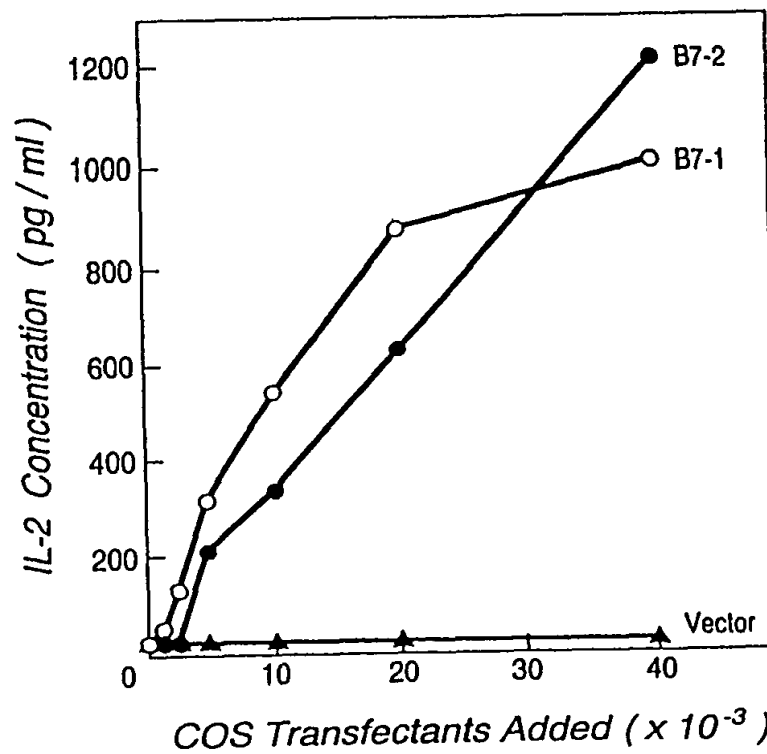


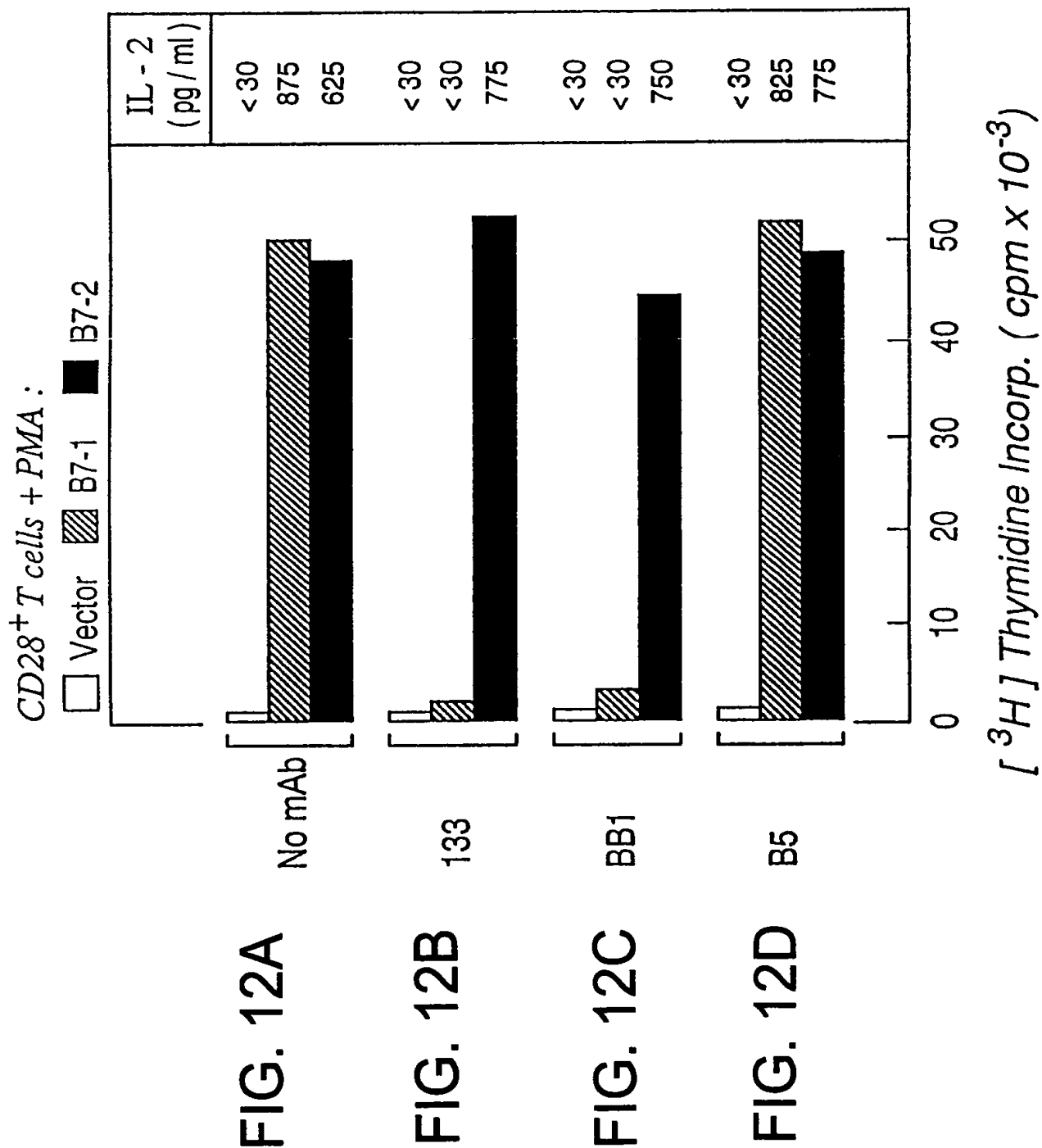
RECEIVED

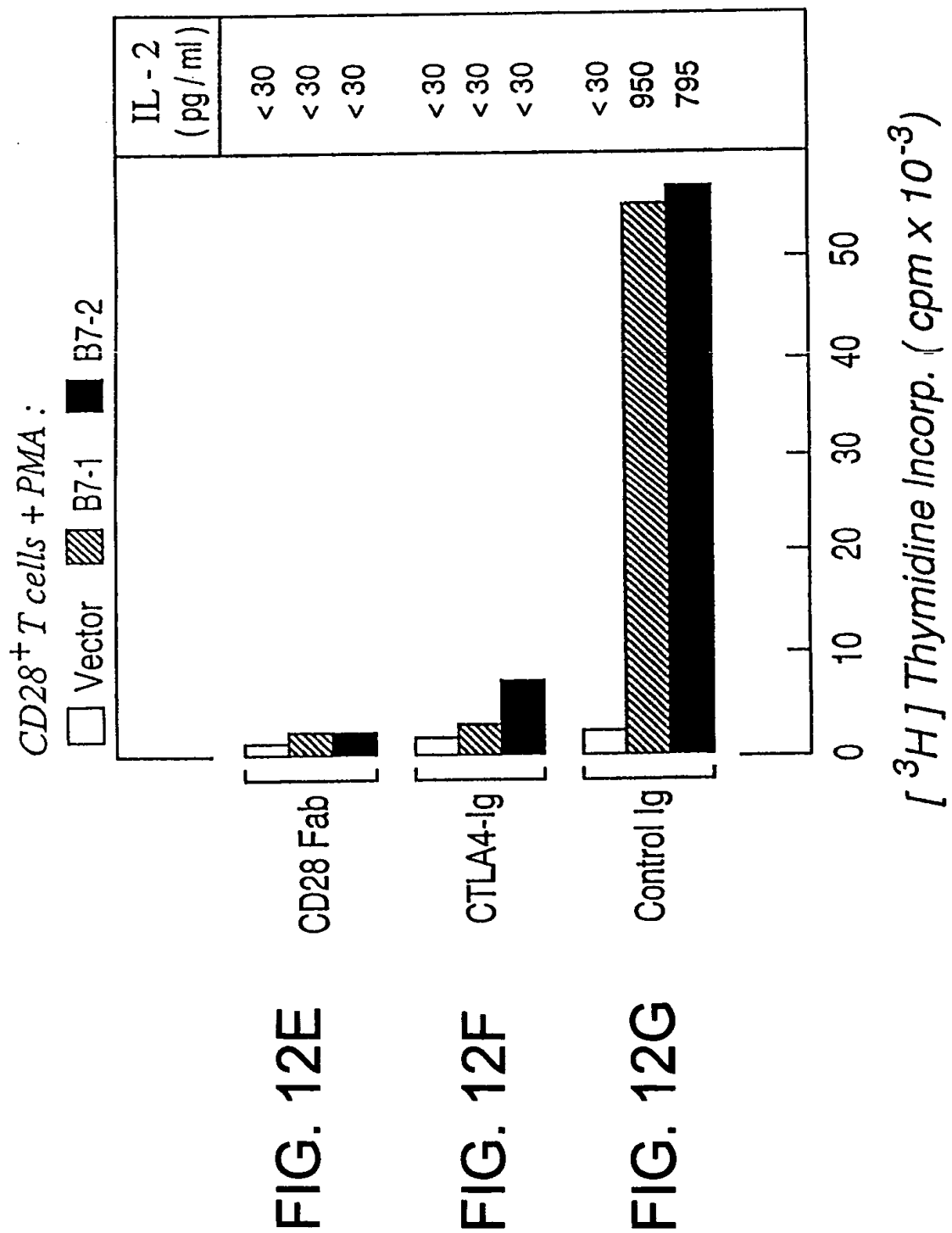
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FIG. 11B







# FIG. 13A

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hB7-1	1	M..GHTRRQGTSPSKCPYLNFQQLLV.LAGLSHFCSGV.IHVTKEVKEVA	46
hB7-2	1	M....DPQCTMGLSN.....ILFVMAFLLSGA...APLKIQAYFNETA	36
mB7	1	MACNCQLMQDTPLLKFPCPRLILLFVLLIRLSQVSSDVDEQLSKSVKDKV	50
		. . . . .	
hB7-1	47	TLSCGHNVSVEE.LAQTRIYWQKEKKMVL.TMSGDMNI...WPEYKNRT	91
hB7-2	37	DLPCQFANSQNQSLSELVFWQDQENLVLNEVYLGKEKFDVHSHSKYMGRT	86
mB7	51	LLPCRY.NSPHEDESEDRIYWQKDKVLS.VIAGKLKV...WPEYKNRT	95
		. . . . .	
hB7-1	92	IFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKAD	141
hB7-2	87	SFD.SDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRIHQMNSLSVLAN	135
mB7	96	LYDN'TT.YSLIILGLVLSDRGTYSVCVVQKKERGTVEVKHLALVLSIKAD	144
		. . . . .	
hB7-1	142	FPTPSISDFEIPTSNI.RRIICSTSGGFPEPH....LSWLENGEELNAIN	186
hB7-2	136	FSQPEIVPISNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGI	185
mB7	145	FSTPNITESGNPSADT.KRITCFASGGFPKPR....FSWLENGRELPGIN	189
		. . . . .	



# FIG. 13B

hB7-1	187	TTVSQDPETELYAVSSKLDEN...MTTNHSEFMCLIKYGHILRVNQTFNWT	233
hB7-2	186	MQKSQDNVTELYDVSISSVSFPDVTSNMTIFCILETDKTRLLSSPFSIE	235
mB7	190	TTISQDPESELYTISSQLDEN...TTRNHTIKCLIKYGDAHVSEDFTWK	236
		. . . . .	
hB7-1	234	TKQEHF.PDNLLPSWAITLISVNGIFVICCLTYCFAPCRERRRNERLRR	282
hB7-2	236	.LEDPPPPDHIPWITAVLP...TVIICVMVFCILILWKWKKKRPRNSY	280
mB7	237	PPEDPPDSKNTLVLFAGFGAVITVVIVVVIKCFCKHRSCFRRNEA.SR	285
		. . . . .	
hB7-1	283	ESVRPV*	288
hB7-2	281	KCG...TNTMERESEQTKKREKIHIPERSDEAQRVFKSSKTSSCDKSDT	327
mB7	286	ETNNSLTFCGPEEALAEQTVFL*	306
		. . . . .	
hB7-2	328	CG*	329

FIG. 14A

1 CCCACGGTCCGGAGCAAGCAGACCGCGTAAGAGTGGCTCCTGTAGGCAGCAGGACTTG  
-----+-----+-----+-----+-----+  
60 GGTGCGCAGGCCCTCGTTCTGCTGCGCATCTCACCGAGGACATCCGTCGTGCCTGAAC

61 AACAAACGACTCCTGTAGACGTGTTCCAGAACTTACGGAAGCACCCACGATGGACCCCA  
-----+-----+-----+-----+-----+  
120 TTGTTGGTCTGAGGACATCTGCACAAGTCTTGAATGCCCTTCGTGGTGCTACCTGGGGT

M D P R -

121 GATGCACCATGGGCTTGGCAATCCTTATCTTTGTGACAGTCTTGCTGATCTCAGATGCTG  
-----+-----+-----+-----+-----+  
180 CTACGTGTACCCGAACCGTTAGGAATAGAAACACTGTGAGAACGACTAGAGTCTACGAC

C T M G L A I L I F V T V L L I S D A V -

181 TTTCGGTGGAGACGCAAGCTTATTTC AATGGGACTGCATATCTGCCGTGCCCATTTACAA  
-----+-----+-----+-----+-----+  
240 AAAGGCACCTCTGCGTTCGAATAAAGTTACCTGACGTATAGACGGCACGGGTAAATGTT

S V E T Q A Y F N G T A Y L P C P F T K -

241 AGGCTCAAAACATAAGCCTGAGTGAGCTGGTAGTATTTTGGCAGGACCAGCAAAAGTTGG  
-----+-----+-----+-----+-----+  
300 TCCGAGTTTGTATTTCGGAATCACTCGACCATCATATAAACCGTCTCTGGTCTGTTTCAACC

A Q N I S L S E L V V F W Q D Q Q K L V -

FIG. 14B

301 TTCTGTACGAGCACTATTGGGCACAGAGAACTTGATAGTGTGAATGCCAAGTACCTGG  
-----+-----+-----+-----+-----+-----+  
AAGACATGCTCGTGATAAACCCGGTGCTCTTTGAACTATCACACTTACGGTTCAATGGACC  
-----+-----+-----+-----+-----+-----+  
L Y E H Y L G T E K L D S V N A K Y L G -  
-----+-----+-----+-----+-----+-----+  
361 GCCGCACGAGCTTTGACAGGAACAACCTGGACTCTACGACTTCACAATGTTTCAGATCAAGG  
-----+-----+-----+-----+-----+-----+  
CGCGTGCTCGAAACTGTCCTTGTGACCTGAGATGCTGAAGTGTACAAAGTCTAGTTCC  
-----+-----+-----+-----+-----+-----+  
R T S F D R N N W T L R L H N V Q I K D -  
-----+-----+-----+-----+-----+-----+  
421 ACATGGGCTCGTATGATGTTTATACAAAAAGCCACCACAGGATCAATTATCCTCC  
-----+-----+-----+-----+-----+-----+  
TGTAACCGAGCATACTAACAAAATATGTTTTTTTCGGTGGTGTCCTAGTTAATAGGAGG  
-----+-----+-----+-----+-----+-----+  
M G S Y D C F I Q K K P P T G S I I L Q -  
-----+-----+-----+-----+-----+-----+  
481 AACAGACATTAAACAGAACTGTCAGTGATCGCCAACTTCAGTGAACCTGAAATAAACTGG  
-----+-----+-----+-----+-----+-----+  
TTGTCTGTAATTGCTTGACAGTCACTAGCGGTTGAAGTCACTTGGACTTTATTTTGACC  
-----+-----+-----+-----+-----+-----+  
Q T L T E L S V I A N F S E P E I K L A -  
-----+-----+-----+-----+-----+-----+  
541 CTCAGAATGTAACAGGAAATCTGGCATAAATTGACCTGCACGTCTAAGCAAGGTCACC  
-----+-----+-----+-----+-----+-----+  
GAGTCTTACATTGTCCTTAAGACCGTATTAAACTGGACGTGCAGATTCCGTTCCAGTGG  
-----+-----+-----+-----+-----+-----+  
Q N V T G N S G I N L T C T S K Q G H P -

FIG. 14C

CGAAACCTAAGAAGATGATATTTCTGATAAACTAATCAACTAATGAGTATGGTGATAACA 660  
601 -----+-----+-----+-----+-----+-----+-----+-----+  
GCTTTGGATTCTTCTACATAAAAGACTATTGATTAAAGTTGATTACTCATACCACCTATTGT

K P K K M Y F L I T N S T N E Y G D N M -  
TGCAGATATCACAAGATAATGTCACAGAACTGTTTCAGTATCTCCAACAGCCTCTCTCTTT  
661 -----+-----+-----+-----+-----+-----+-----+  
ACGTCATAGTGTCTATTACAGTGTCTTGACAAGTCATAGAGGTTGTCGGAGAGAGAAA

Q I S Q D N V T E L F S I S N S L S L S -  
CATTCGCCGATGGTGTGGCATAATGACCGTTGTGTGTCTGGAACGGAGTCAATGA 780  
721 -----+-----+-----+-----+-----+-----+-----+  
GTAAGGCGCTACCACACACCGTATATACTGGCAACACACACAGACCTTTGCCCTCAGTTACT

F P D G V W H M T V V C V L E T E S M K -  
AGATTTCCTCCAACCTCTCAATTTCACTCAAGAGTTTCCATCTCCTCAAACGTATTGGA 840  
781 -----+-----+-----+-----+-----+-----+-----+  
TCTAAAGGAGGTTTGGAGAGTTAAAGTGAGTTCTCAAAGGTAGAGGAGTTTGCTATAACCT

I S S K P L N F T Q E F P S P Q T Y W K -  
AGGAGATTACAGCTTCAGTTACTGTGGCCCTCCTCCTTGTGATGCTGCTCATCTGTAT 900  
841 -----+-----+-----+-----+-----+-----+-----+  
TCCTCTAATGTCGAAGTCAATGACACCGGAGGAGGAACACTACGACGAGTAGTAACATA

E I T A S V T V A L L L V M L L I I V C -

FIG. 14D

901 GTCACAAGAACCGAATCAGCCTAGCAGGCCAGCAACACAGCCCTCTAAGTTAGAGCGGG  
-----+-----+-----+-----+-----+-----+ 960  
CAGTGTCTTCGGCTTAGTCGGATCGTCCGGGTCGTTGTGTGTCGAGATTCAATCTCGCCC

H K K P N Q P S R P S N T A S K L E R D -

961 ATAGTAACGCTGACAGAGAGACTATCAACCTGAAGAACTTGAACCCCAAAATTGCTTCAG  
-----+-----+-----+-----+-----+-----+ 1020  
TATCATTCGCACTGTCTCTGATAGTTGACTTCCTTGAACCTTGGGGTTTAAACGAAGTC

S N A D R E T I N L K E L E P Q I A S A -

1021 CAAAACCAATGCAGAGTGAAGGCAGTGAGAGCCTGAGGAAAGAGTTAAAAATTGCTTTG  
-----+-----+-----+-----+-----+-----+ 1080  
GTTTGGTTTACGTCTCACTCCGTCACCTCTCGGACTCCTTCTCAATTTTAAACGAAAC

K P N A E \*

1081 CCTGAAATAAGAAGTCAGAGTTTCTCAGAATTCAAAAATGTTCTCAGCTGATTGGAATT  
-----+-----+-----+-----+-----+-----+ 1140  
GGACTTTATTCTTCACGTCTCAAAGAGTCTTAAAGTTTTCACAGAGTCGACTAACCTTAA

CTACAGTTGAATAATTAAAGAAC  
1141 -----+-----+----- 1163  
GATGTCAACTTATTAAATTCTTG

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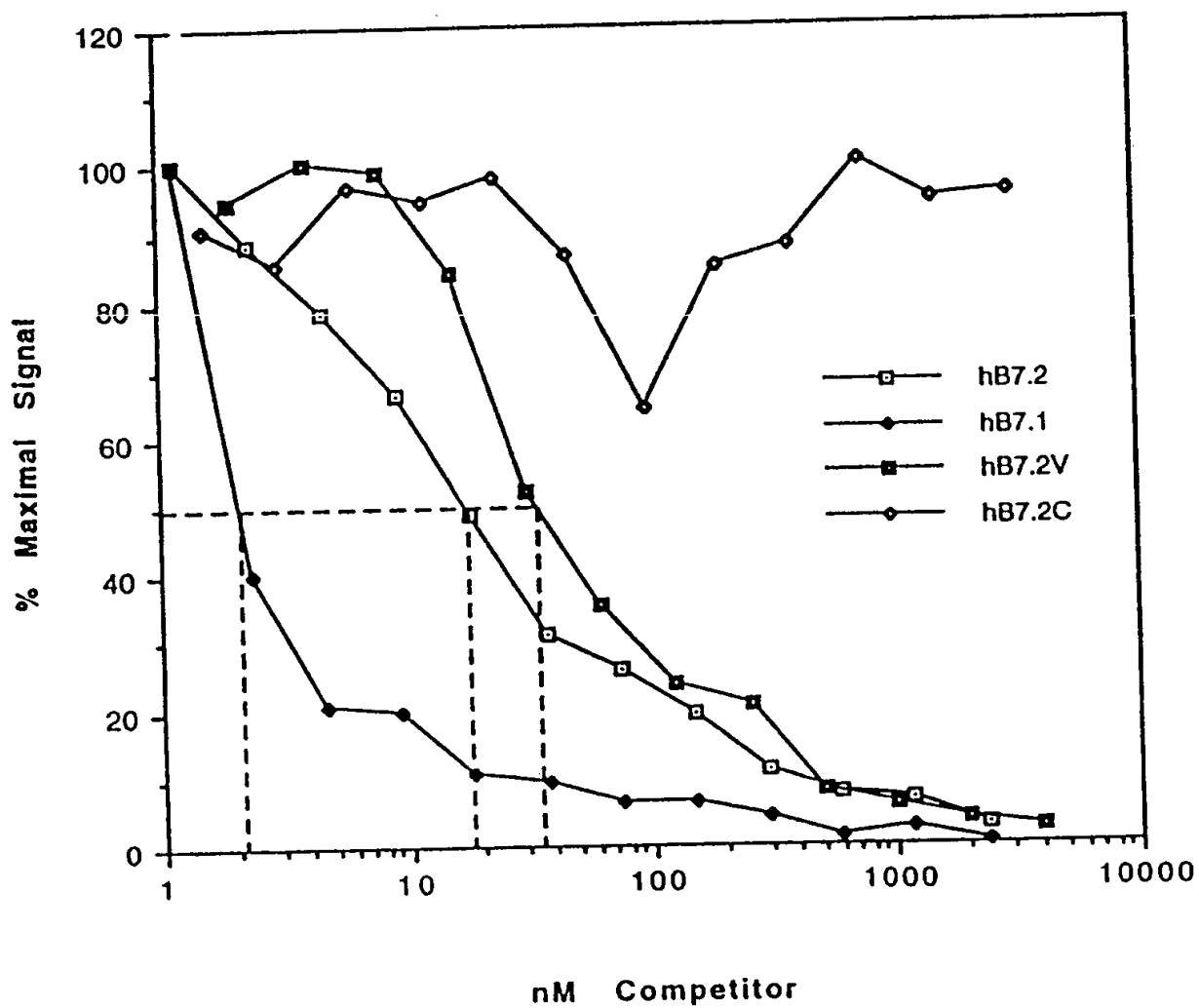


FIG. 15

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FIG. 16A

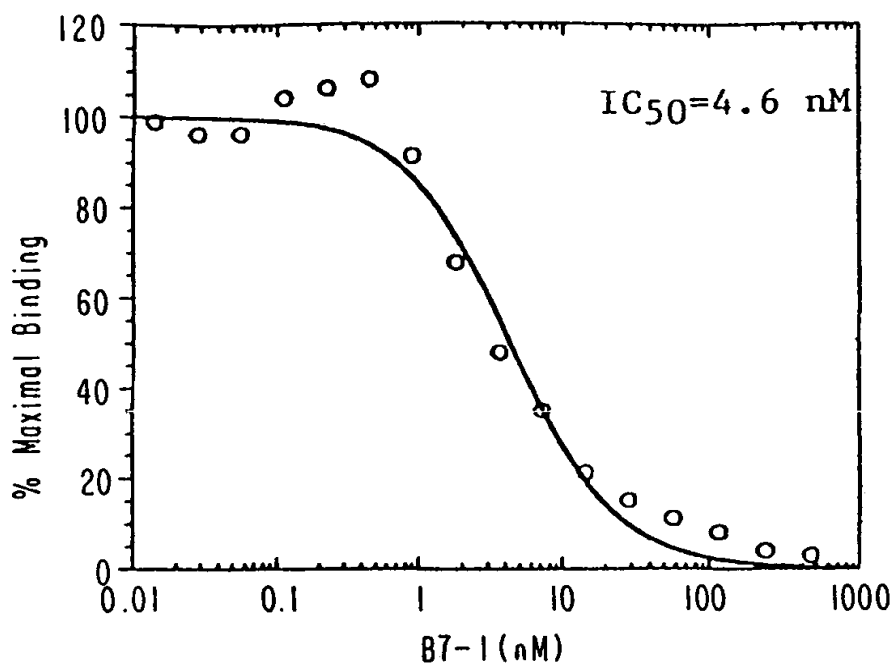


FIG. 16B

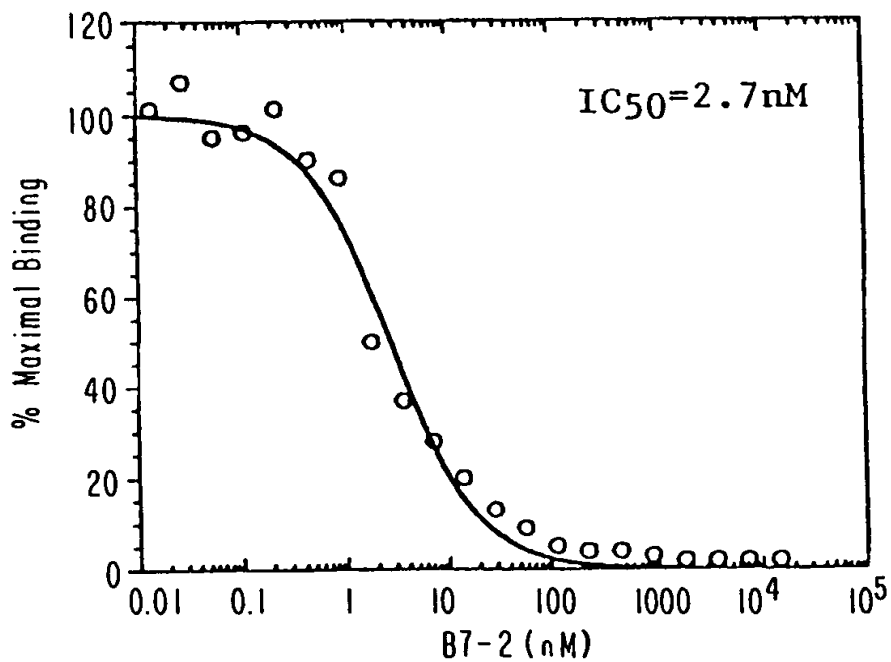


FIG. 17A

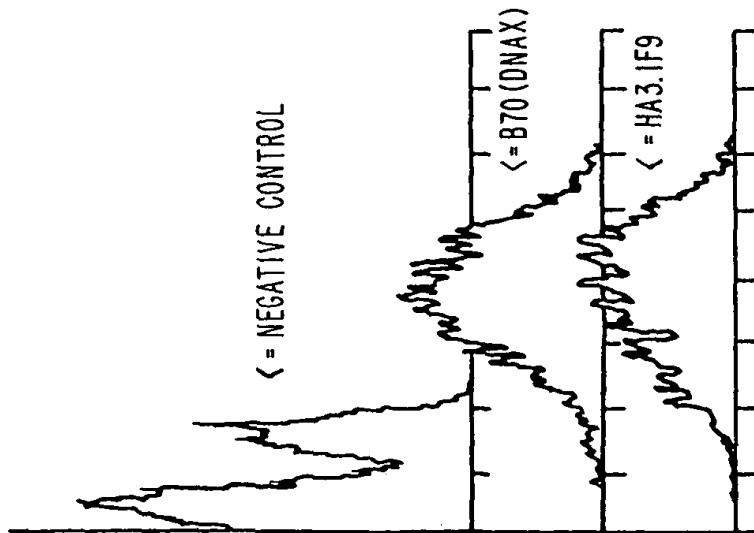


FIG. 17B

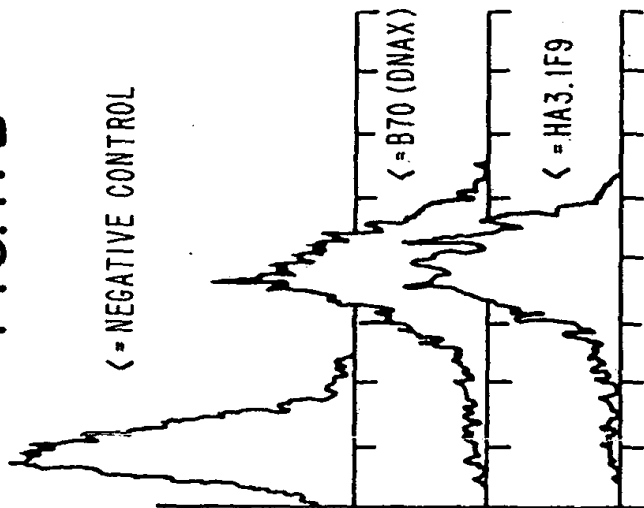


FIG. 17C

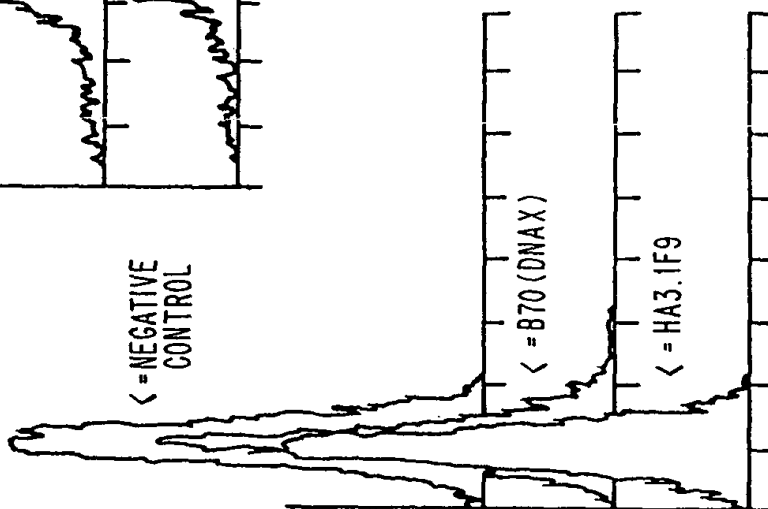




FIG. 18B

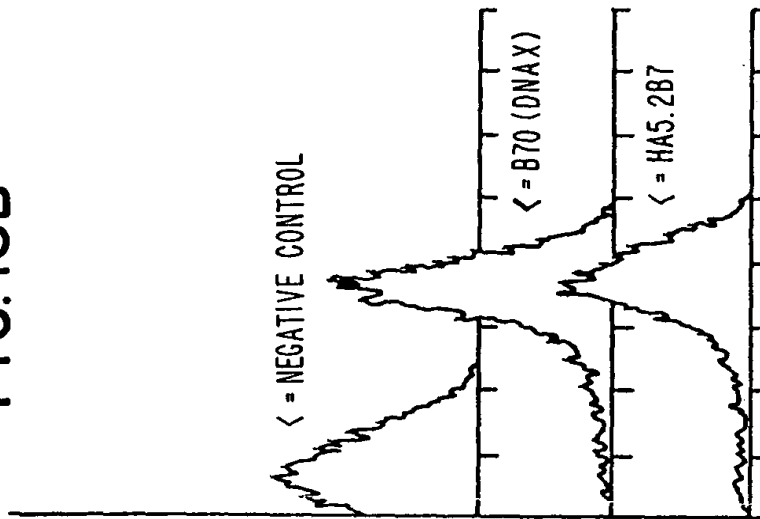


FIG. 18C

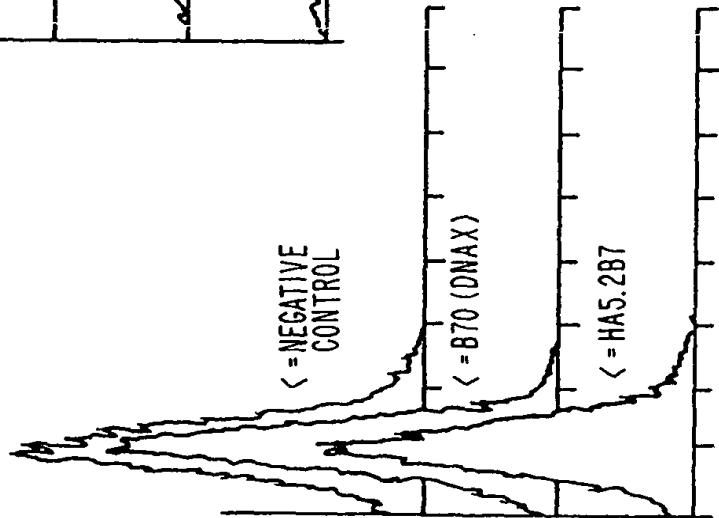


FIG. 18A

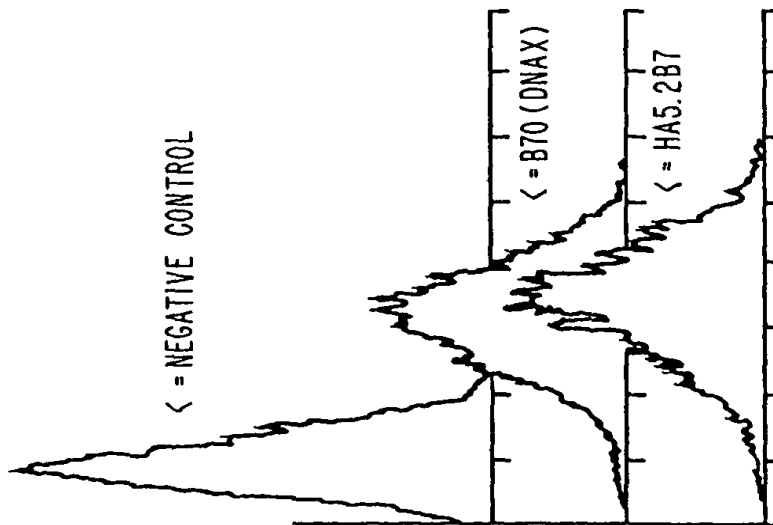


FIG. 19A

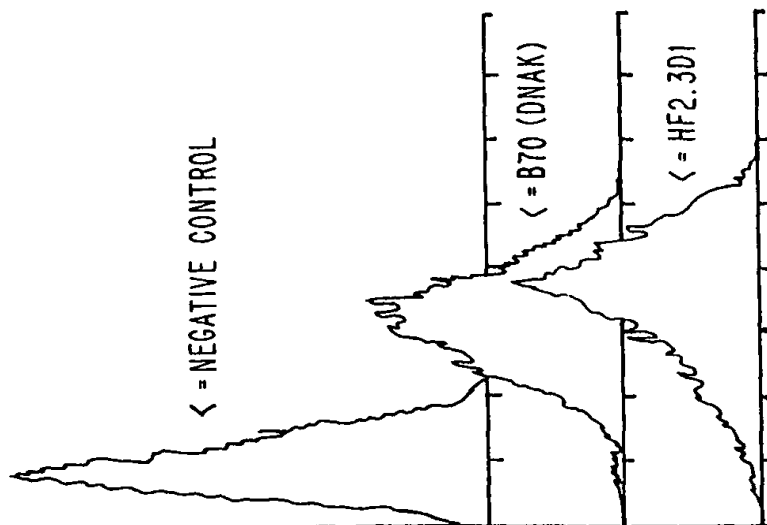


FIG. 19C

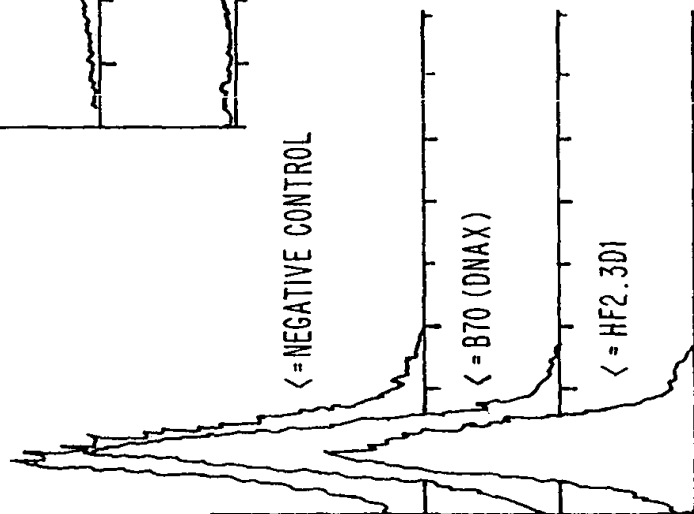


FIG. 19B

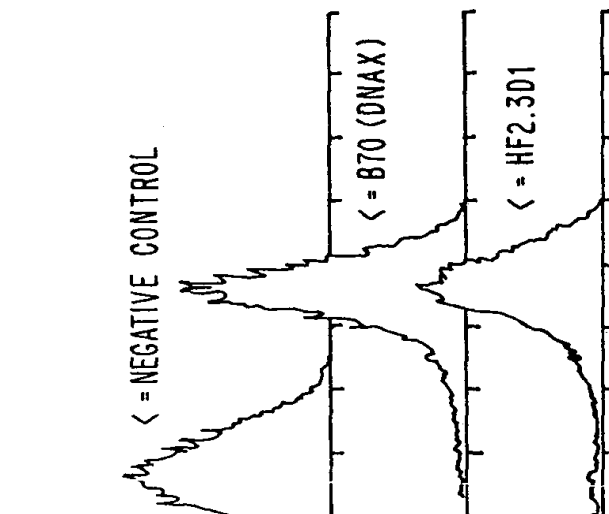
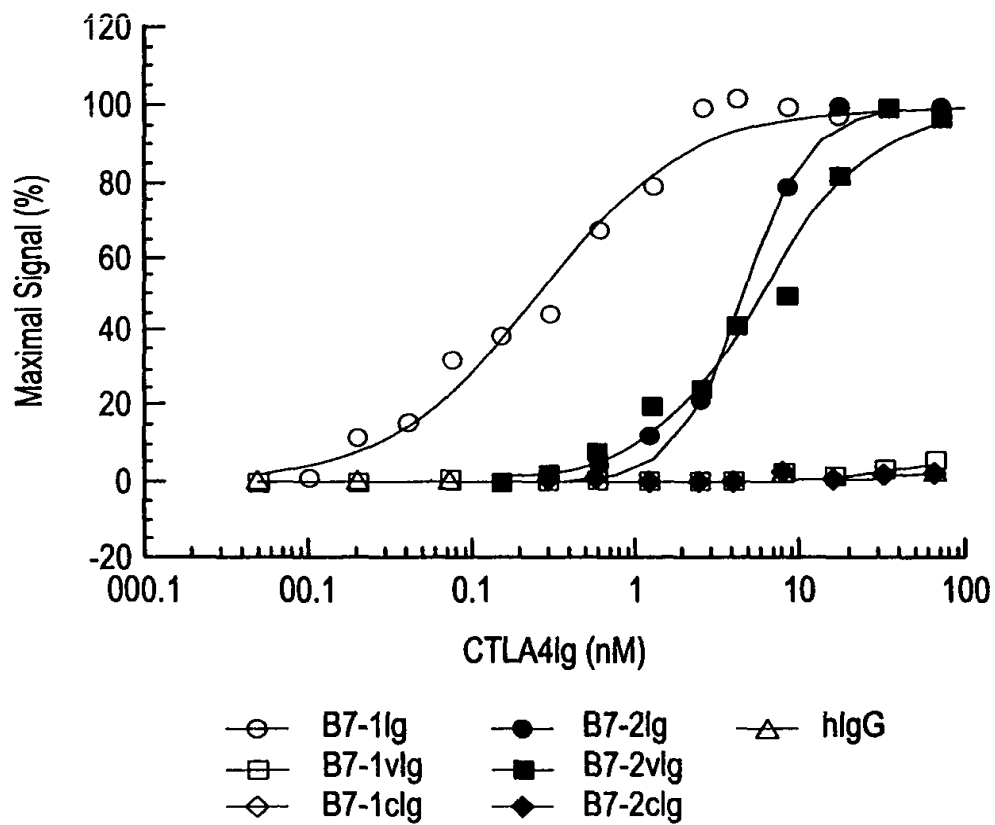


FIG. 20



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FIG. 21A

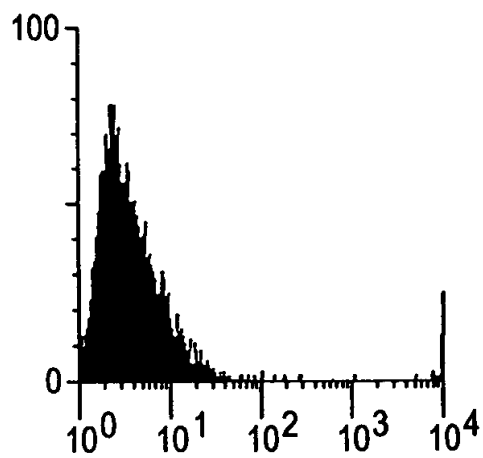


FIG. 21B

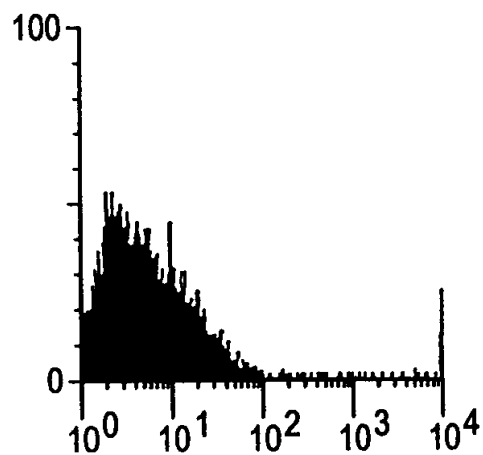


FIG. 21C

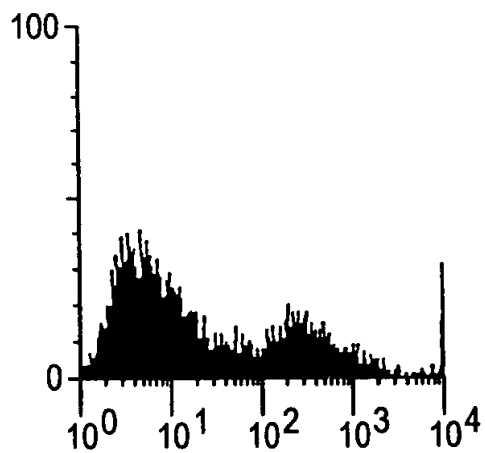


FIG. 21D

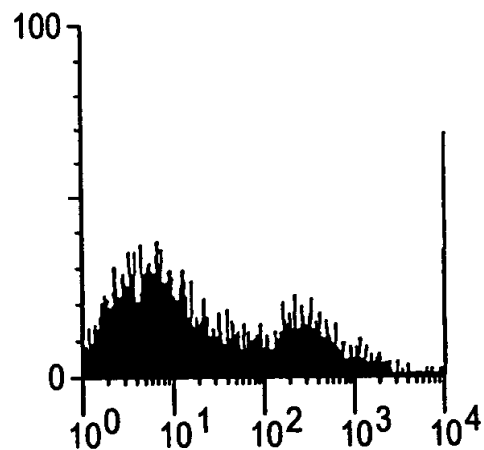


FIG. 21E

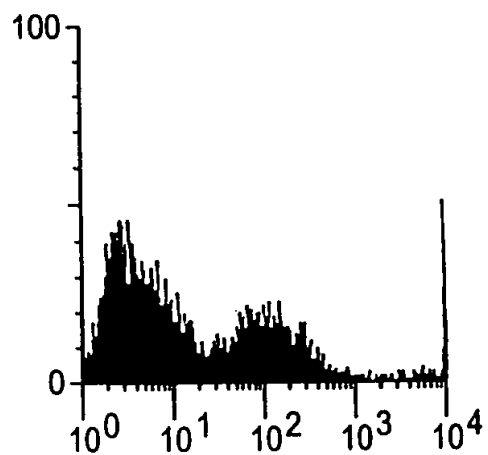


FIG. 22

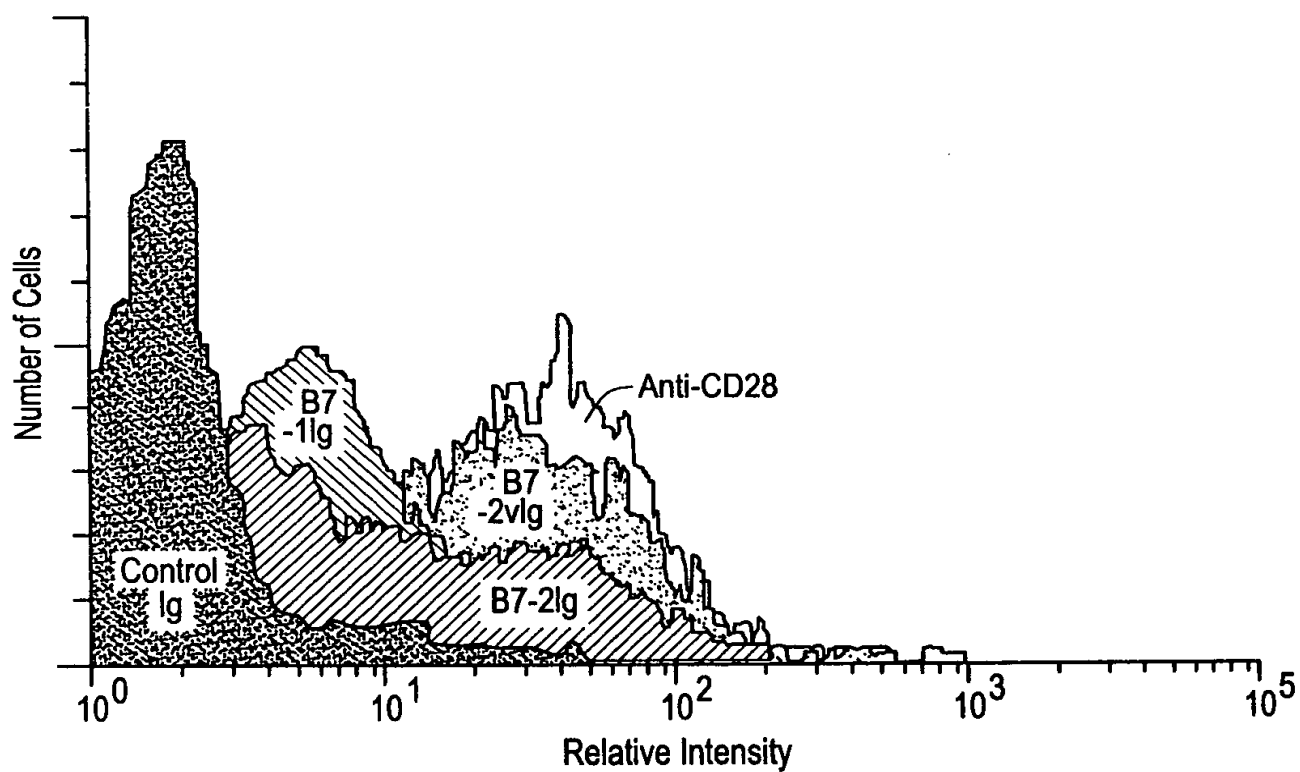


FIG. 23

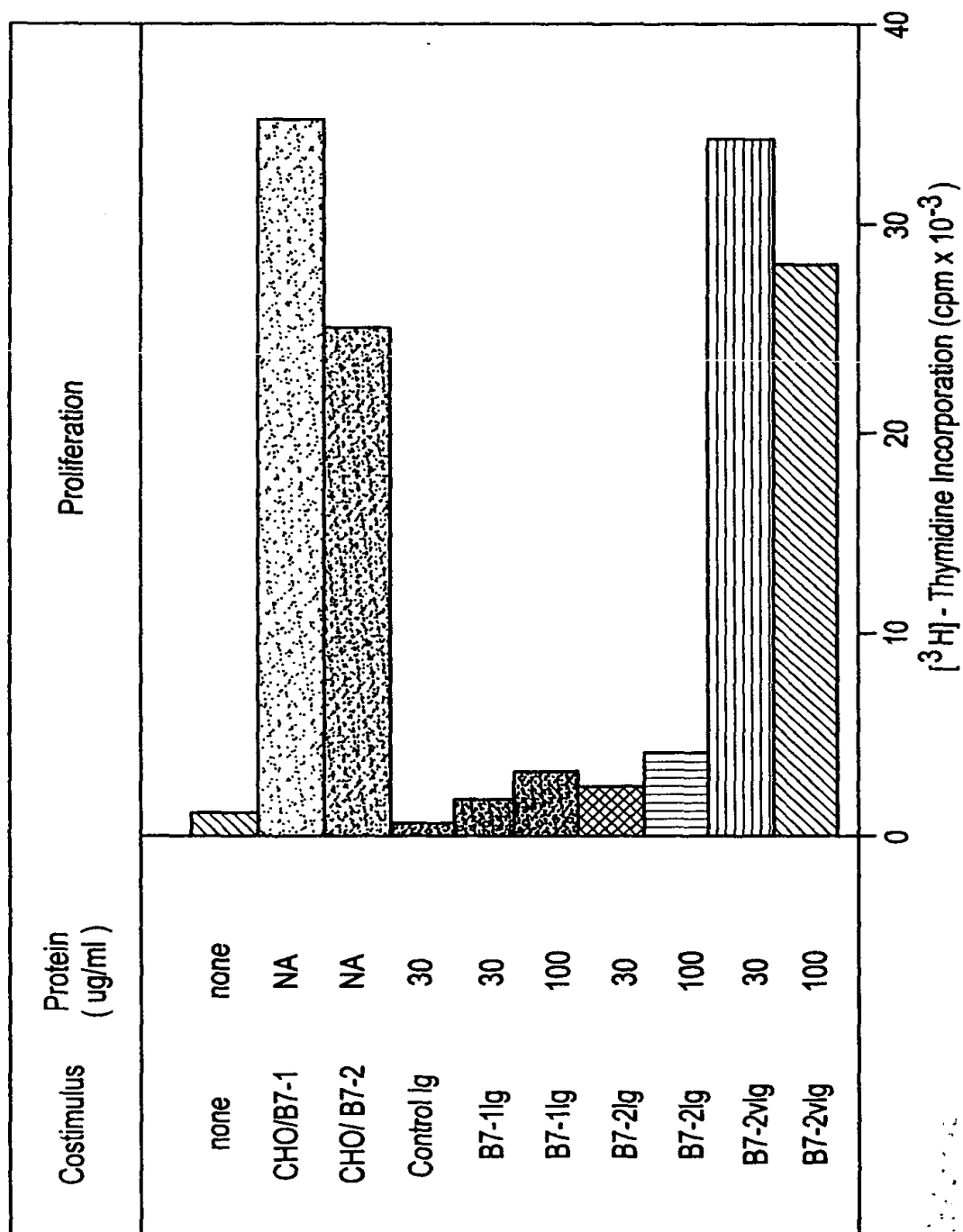


FIG. 24

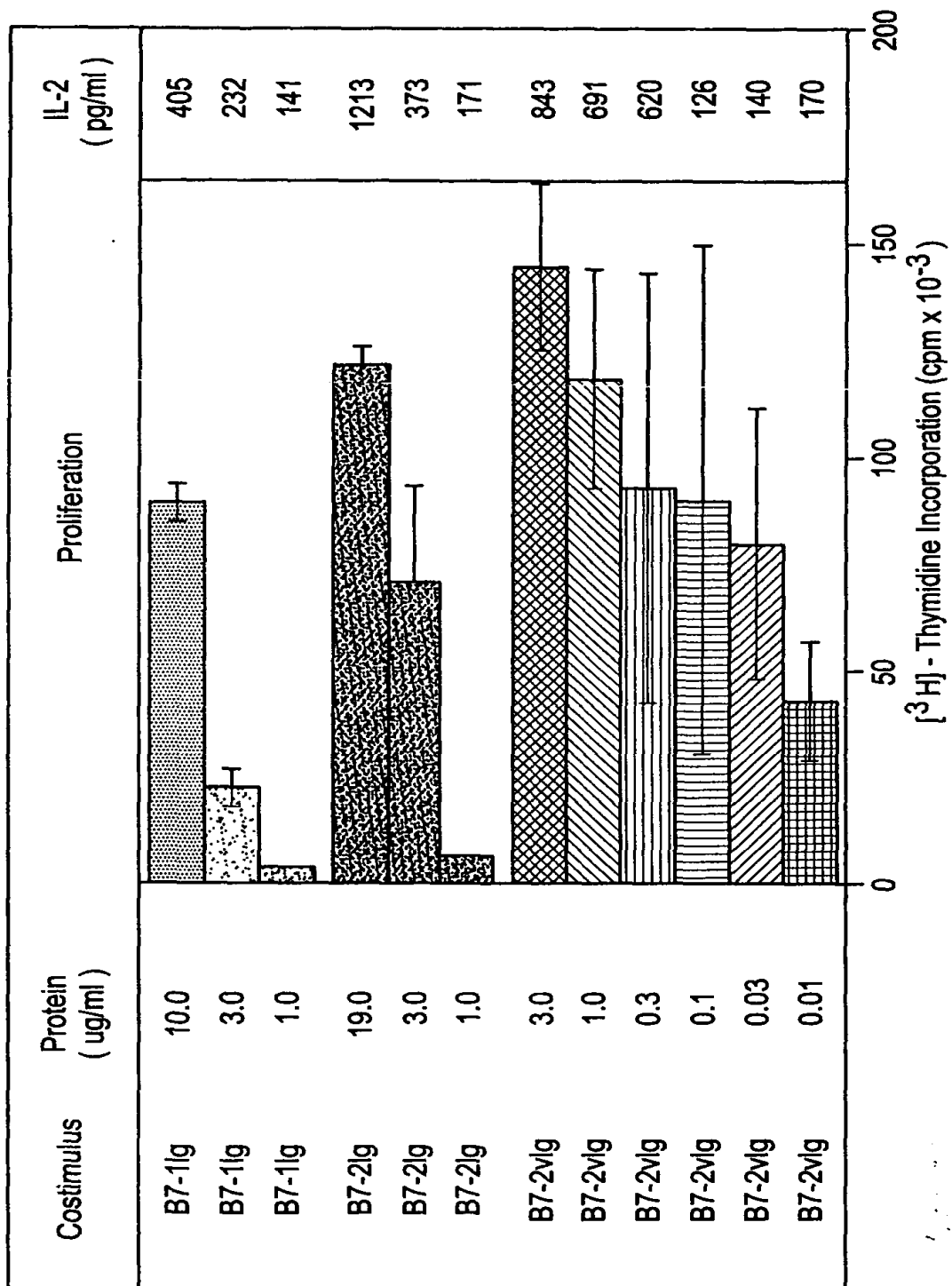


FIG. 25

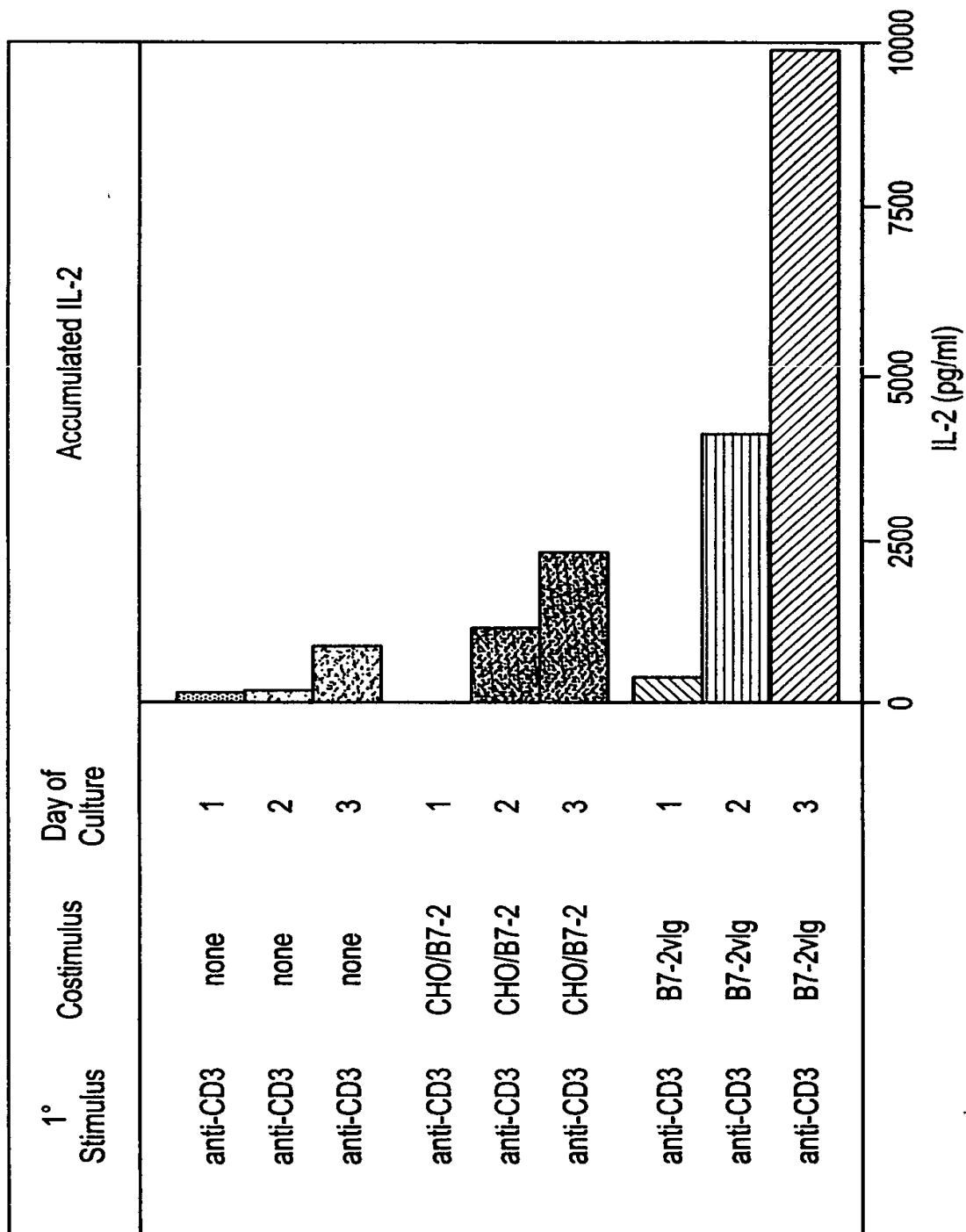




FIG. 26

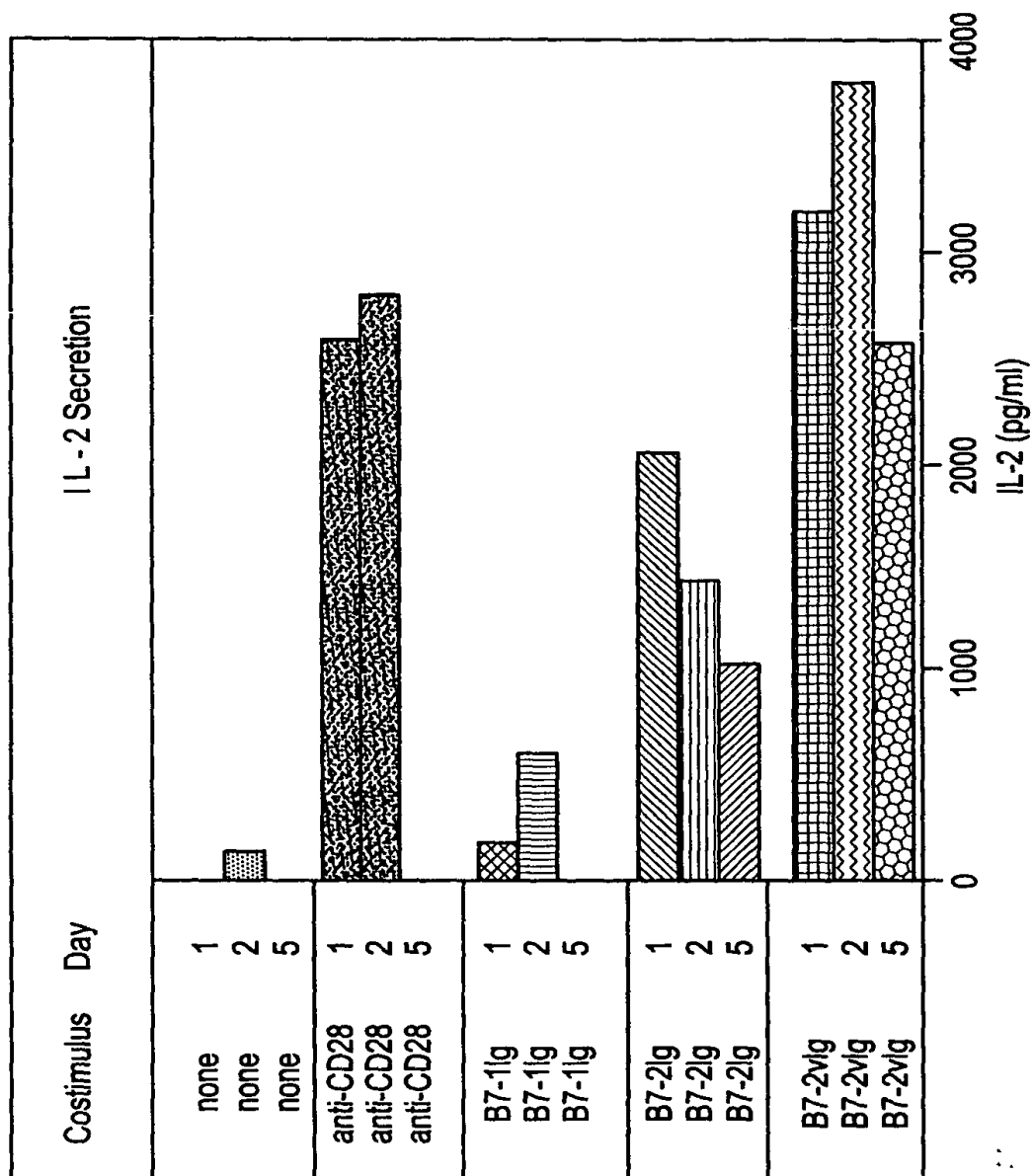


FIG. 27

